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RAW SEQUENCE LISTING

DATE: 09/24/2002

PATENT APPLICATION: US/10/092,947

TIME: 11:16:09

Input Set : N:\Crf4\09232002\J092947.raw

Output Set: N:\CRF4\09242002\J092947.raw

1 <110> APPLICANT: WOLFF, Anne M
 2 APPEL, Karen F
 3 PETERSEN, Jesper F
 4 POULSEN, Ulla
 5 ARNAU, Jose
 6 JACOBSEN, Mette D
 7 <120> TITLE OF INVENTION: MUCOR RECOMBINANT GENE EXPRESSION
 8 <130> FILE REFERENCE: WOLFF=3
 9 <140> CURRENT APPLICATION NUMBER: US/10/092,947
 10 <141> CURRENT FILING DATE: 2002-03-08
 11 <150> PRIOR APPLICATION NUMBER: US 60/274,650
 12 <151> PRIOR FILING DATE: 2001-03-12
 13 <160> NUMBER OF SEQ ID NOS: 65
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2525
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Mucor circinelloides
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 23 <223> OTHER INFORMATION: Exon of pkar
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 27 <223> OTHER INFORMATION: n is a, c, g or t
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 42 <222> LOCATION: (1708)..(1760)
 43 <223> OTHER INFORMATION: Intron of pkar
 44 <400> SEQUENCE: 1

Does Not Comply
Corrected Diskette Needed

pp. 4-8

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45 aagctttatt catttcactg gtcaacgtaa gtacatttct ctcagtattg gtcgctttta 60
46 tatcatcttt ttggctgctt tacgtgatga acaaaacatt atgctactaa acccagctca 120
47 gtttgagata ttcggtgaaa gaaactatct ccataactga aaaagttaaa ccaaaaagat 180
48 atatgaaaat gatacattta cttgttcatt tgagctccat attaatactc ttctcctcta 240
49 gttggcatgt ctttttgcaa gccaaaagcta cctatagctc aggtctatta gatgtatcat 300
50 cttgatcttt ttggaattga ataaataaat ttcttgatt ttaaaatgta acactttaat 360
51 gcctaatttc tgcgtgcaat gtcgtttttt ttctgtgat aacctgaac tgcctaaatg 420
52 ctttcatgat gtcactcat aatctgttg gttacatcca atactgttaa attgtatgtg 480
53 ttgatcttga gtataaggga tcgatcattt gattgtcttt ttctcctcta ttttcattaa 540
54 a atg atc act gac gaa cat ccg ttt gaa ttt gcg cct cag caa gat gaa 589
55 Met Ile Thr Asp Glu His Pro Phe Glu Phe Ala Pro Gln Gln Asp Glu
56 1 5 10 15
57 tac acg cag ctg ttg aca gag tta cat aac gaa tac tgc gct gag caa 637
58 Tyr Thr Gln Leu Leu Thr Glu Leu His Asn Glu Tyr Cys Ala Glu Gln
59 20 25 30
60 cca cta gat gtg ctt cag ttc tgc tcc aac ttt ttc att cgc aaa ctc 685
61 Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu
62 35 40 45
63 gaa gag cag cgc ttg gag cat aga aac aac cac cat tcc cgtaacaact 734
64 Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser
65 50 55 60
66 tgtttgatag taaagtgtct ctgccacgag cctagtgatg gatgctaacg tttttcctta 794
W--> 67 g ccn aat gat acc agt aat gat tta cat cct ttg tgt gag caa cca caa 843
68 Pro Asn Asp Thr Ser Asn Asp Leu His Pro Leu Cys Glu Gln Pro Gln
69 65 70 75
70 gaa gac ttt tca caa cag caa ggc atc cag tgg gaa acc acg cat atg 891
71 Glu Asp Phe Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr Thr His Met
72 80 85 90
73 ggc cat ccc aac gac cac ggt gct ctt cat gat gat gat gat gat ccg 939
74 Gly His Pro Asn Asp His Gly Ala Leu His Asp Asp Asp Asp Asp Pro
75 95 100 105
76 ttg gaa gac gaa gac gat gaa gag ttt gac aaa ttt tca act gaa cct 987
77 Leu Glu Asp Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser Thr Glu Pro
78 110 115 120 125
79 ttg ccc tcg ctg cct ccc aca aac tat aac cgt ggc cgc cgc aca tct 1035
80 Leu Pro Ser Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg Arg Thr Ser
81 130 135 140
82 gtt aag tgc aga gag cat ggc acc cag cgc caa cca aga ctt tgt caa 1083
83 Val Lys Cys Arg Glu His Gly Thr Gln Arg Gln Pro Arg Leu Cys Gln
84 145 150 155
85 ggt cat cat ccc caa atc tca ggc aca agc gag cgc atc aaa gtc tcc 1131
86 Gly His His Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile Lys Val Ser
87 160 165 170
88 atc agc aac aac ttt ttg ttt cgc aac ctg gac gaa gag cag tac ctg 1179
89 Ile Ser Asn Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu Gln Tyr Leu
90 175 180 185
91 gat gtg gtg aat gcc atg tct gaa aag cgc gtc gtc aag ggc acc aca 1227
92 Asp Val Val Asn Ala Met Ser Glu Lys Arg Val Val Lys Gly Thr Thr
93 190 195 200 205

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94	gtg atc gag caa ggc agt gtg ggt gat ttc ttc tac gtc gtc gag tcg	1275
95	Val Ile Glu Gln Gly Ser Val Gly Asp Phe Phe Tyr Val Val Glu Ser	
96	210 215 220	
97	ggt act ttg gat tgt ttt att ggg caa aac aag gtt acc aac tat gag	1323
98	Gly Thr Leu Asp Cys Phe Ile Gly Gln Asn Lys Val Thr Asn Tyr Glu	
99	225 230 235	
100	gca ggt ggt agc ttc ggt gaa tta gcc tta atg tac aac gcc cct cgt	1371
101	Ala Gly Gly Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg	
102	240 245 250	
103	gct gct act att att aca aca tca gac tct gtg ctt tgg gct ctg gac	1419
104	Ala Ala Thr Ile Ile Thr Thr Ser Asp Ser Val Leu Trp Ala Leu Asp	
105	255 260 265	
106	aga aac act tcg gca cca tcc ttg atg gag aac acc tca cgc aaa aga	1467
107	Arg Asn Thr Ser Ala Pro Ser Leu Met Glu Asn Thr Ser Arg Lys Arg	
108	270 275 280 285	
109	cgc atg tat gaa tac ttc tta tca gaa gtc gtc ttg tta aaa tcc ctg	1515
110	Arg Met Tyr Glu Tyr Phe Leu Ser Glu Val Val Leu Leu Lys Ser Leu	
111	290 295 300	
112	gaa tca tat gaa cag cat aaa att gcg gat gcc ctc gaa tca gtt tat	1563
113	Glu Ser Tyr Glu Gln His Lys Ile Ala Asp Ala Leu Glu Ser Val Tyr	
114	305 310 315	
115	ttt gaa gat gga cag gag gtt gtg aag cag ggt gat gtc gga gat cag	1611
116	Phe Glu Asp Gly Gln Glu Val Val Lys Gln Gly Asp Val Gly Asp Gln	
117	320 325 330	
118	ttc tac atc att gaa tcc ggt gaa gcc atc gtc ctg aag gaa gag aac	1659
119	Phe Tyr Ile Ile Glu Ser Gly Glu Ala Ile Val Leu Lys Glu Glu Asn	
120	335 340 345	
121	ggc gtc cag caa cag gtg aac cag ctt gag cga gga tcc tac ttt gga	1707
122	Gly Val Gln Gln Gln Val Asn Gln Leu Glu Arg Gly Ser Tyr Phe Gly	
123	350 355 360 365	
124	ggtaagatgg agcttggtgg ggttggtgat gtgtcgctaa ccactgtgtg ata gaa	1763
125	Glu	
126	ctg gcc ctg tta aac gat gct cct cga gct gca acc gta gtt gct cac	1811
127	Leu Ala Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr Val Val Ala His	
128	370 375 380	
129	ggc aga ctc aag tgc gct aca ctg ggc aaa aag gca ttc act cgt ctt	1859
130	Gly Arg Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu	
131	385 390 395	
132	ctt ggc cct gtt ttg gac atc ttg aag cgt aat tca gaa aac tat cat	1907
133	Leu Gly Pro Val Leu Asp Ile Leu Lys Arg Asn Ser Glu Asn Tyr His	
134	400 405 410	
135	gct gtc att aac cag caa tca taatcgacc aaaaagttac actagatttc	1958
136	Ala Val Ile Asn Gln Gln Ser	
137	415 420	
138	aaataaaaac catggatact ttccgatctg atgttgactt gactgtaaca aagcgacagg	2018
139	aaaaagaaac ttgatttgct tcctgaccaa caatgcagcc aatctcctta aacaagatgc	2078
140	tctctatttc ggctgaaaa tataacctcc ttgatttcgt attttgktgt tgtgcttttt	2138
141	tcctctctc tctctcttc ttttactct tggtataaaa aaaatatgac gggtatgatt	2198
142	cacagtatgg agagcaaccc ttgatgagcc tccacctcaa agcgccagcg gcctcttcta	2258

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143 atctgcctgg cacaggtatt gccaatctac caaatcaaag acacaagatt gttgcaaaa 2318
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145 gaccaggtaa ctgaattttg cttagggtgaa tcgggtgtcg gaaaaacaac ctttgtaa 2438
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162 Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu
163 35 40 45
164 Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser Pro Asn Asp
165 50 55 60
166 Thr Ser Asn Asp Leu His Pro Leu Cys Glu Gln Pro Gln Glu Asp Phe
167 65 70 75 80
168 Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr His Met Gly His Pro
169 85 90 95
170 Asn Asp His Gly Ala Leu His Asp Asp Asp Asp Asp Pro Leu Glu Asp
171 100 105 110
172 Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser Thr Glu Pro Leu Pro Ser
173 115 120 125
174 Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg Arg Thr Ser Val Lys Cys
175 130 135 140
176 Arg Glu His Gly Thr Gln Arg Gln Pro Arg Leu Cys Gln Gly His His
177 145 150 155 160
178 Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile Lys Val Ser Ile Ser Asn
179 165 170 175
180 Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu Gln Tyr Leu Asp Val Val
181 180 185 190
182 Asn Ala Met Ser Glu Lys Arg Val Val Lys Gly Thr Thr Val Ile Glu
183 195 200 205
184 Gln Gly Ser Val Gly Asp Phe Tyr Val Val Glu Ser Gly Thr Leu
185 210 215 220
186 Asp Cys Phe Ile Gly Gln Asn Lys Val Thr Asn Tyr Glu Ala Gly Gly
187 225 230 235 240
188 Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg Ala Ala Thr
189 245 250 255
190 Ile Ile Thr Thr Ser Asp Ser Val Leu Trp Ala Leu Asp Arg Asn Thr
191 260 265 270
192 Ser Ala Pro Ser Leu Met Glu Asn Thr Ser Arg Lys Arg Arg Met Tyr

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*delete - "n" is only shown
in a nucleotide*

sequence

*Please
delete
any
similar
errors
in subsequent
sequences*

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Input Set : N:\Crf4\09232002\J092947.raw
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197    305          310          315          320
198    Gly Gln Glu Val Val Lys Gln Gly Asp Val Gly Asp Gln Phe Tyr Ile
199          325          330          335
200    Ile Glu Ser Gly Glu Ala Ile Val Leu Lys Glu Glu Asn Gly Val Gln
201          340          345          350
202    Gln Gln Val Asn Gln Leu Glu Arg Gly Ser Tyr Phe Gly Glu Leu Ala
203          355          360          365
204    Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr Val Val Ala His Gly Arg
205          370          375          380
206    Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu Leu Gly
207    385          390          395          400
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240    1          5          10          15
241    tcg cct tca tct caa aca arn atg gac gat ttt gaa atc aaa cag cca      96
242    Ser Pro Ser Ser Gln Thr Xaa Met Asp Asp Phe Glu Ile Lys Gln Pro

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